



MAR 0 4 2003



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RAW SEQUENCE LISTING

FATENT APPLICATION: US/09/645,337A

DATE: 02/27/2003 TIME: 10:31:45

Input Set : A:\104107.01.txt

Output Set: N:\CRF4\02272003\I645337A.raw

```
3 <110> APPLICANT: Wu, Kegiang
       - Miki, Brian L
        Tian, Lining
        Brown, Dan
8 <120> TITLE OF INVENTION: Repressing Gene Expression in Plants
10 <130> FILE REFERENCE: 104107.1
12 <140> CURRENT APPLICATION NUMBER: US 09/645,337A
13 <141> CURRENT FILING DATE: 2000-08-25
15 <150> PRIOR APPLICATION NUMBER: US 09/383,971
16 <151> PRIOR FILING DATE: 1999-08-27
18 <160> NUMBER OF SEQ ID NOS: 14
20 <170> SOFTWARE: PatentIn version 3.2
22 <210> SEC ID NO: 1
23 <211> LENGTH: 1807
24 <212> TYPE: DNA
25 <213> ORGANISM: Arabidopsis thaliana
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                                                                          120
32 tgatoctacg aaaaagaggt aatggatact ggoggcaatt ogotggogto oggacotgat
                                                                          180
34 ggtgtgaaga ggaaagtttg ttatttetat gaeeetgagg teggeaatta etaetatgge
                                                                          240
                                                                          300
36 caaggicate ceatgaagee ceategeare egeatgacee atgeecteet egereactae
38 ggtotoctto agcatatgoa ggttotoaag coottoootg coogogaacg tgatototgo
                                                                          360
40 cycticcacy cegacyacta tytotottit cicegoagea tiaccectga aacceageaa
                                                                          420
                                                                          480
42 gatcagattc gccaacttaa gcgcttcaat gttggtgaag actgtcccgt ctttgacggc
44 cfttattcct tftgedagad diatgetgga ggaldtgttg gtggetctgt däagdttaad
                                                                          540
46 cacggedtet gegatatige cateaactgg getggiggie tecateacge taagaagige
                                                                          600
48 gaggeetetg geitetgita egicaatgal alegietiag elaleetaga geleettaag 👚
                                                                          660
                                                                          720
50 caqcatgago gtgttottta tqtogatatt gatatocaco acqqqqatgg aqtggaqqa -
52 geatittatg ctactgacag ggttatgact giclogitte afaaattigg tgattactti -
                                                                          780
54 eccqqtacaq qteacattca qqatataqqt tatqqtaqcq qaaaqtacta ttetetcaat -
                                                                          840
56 glaccactgg atgatggaat ogatgatgag agctatoato tgttattcaa gcccatcatg
                                                                          900
58 gggaaagtta tggaaatttt oogaddaggg gotgtggtat tgdaatgtgg tgotgactoo
                                                                          960
                                                                         1020
60 ctatctgggg aloggttagg tigottcaat ctitcaatca aaggtcatgo tgagtgcgto
62 aaatttatga gategtteaa tyttooceta etgetettyy ytyytyy ttacaetate
                                                                         1080
64 ogcaatgitg deegtigeig gigetacgag aciggagitg cacitggagi igaagitgaa
                                                                         1140
                                                                        1200
66 gacaaqatgo oggagoarga atattatgaa tactitiggio cagactarac acticacgit -
68 getecaagta adatggaaaa taagaattot ogreagatgo tigaagagat togeaatgad -
                                                                        1260
70 ctintegada atotototaa gottoagoat ootonaagtg tacdattina ggaaagadda \simeq 1320
72 ortgatanag agadtonoga ggttgatgaa gannaagaag alggggataa aagatgggat -
                                                                        1380
94. eregdat bead lacat ggat gtillt gat gat gat egbalaetet i i barktalageag lägt adlalägga.
                                                                        1440
VK (palapot gtil di laasma gatlam laala kkamalang diat qda int da laad galat tiat ilig ka googtigga).
                                                                         11.11
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De aalagditigtig ladgiig ragji lipjat dadagi lipjaagka italiaggiita tagjilagtaaakkida.

1560

RAW SEQUENCE LISTING

FATERY AFFLECATION: US/09/645,337A TIME: 10:31:45

DATE: 0272777003

Input Set : A:\104107.01.txt

Output Set: N:\CRF4\02272003\I645337A.raw

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96 <400> SEÇ 98 Met Asp 1			Ser L	eu I	∖la S	Ger (aly I	Pro A	Asp (_ys	
99 1 102 Arg Lys			Tyr	Asp		EO Glu	Val	Gly	Asn		15 Tyr	Tyr	
103 106 Gly Gln 107	20 Gly His 35	Pro Met	Lys	Pro 40		Arg	Ile	Arg	Met 45	-	His	Ala	
110 Leu Leu 111 50		Tyr Gly	Leu 55		Gln	His	Met	Gln 60	Val	Leu	Lys	Pro	
114 Phe Pro 115 65		70					75					80	
118 Val Ser 119		85				90					95		
122 Arg Gln 123	100				105					110			
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130 Ser Val 131 130			135					140					
134 Gly Gly 135 145		150					155					160	
138 Val Asn 139		165				170					175		
142 Arg Val 143	180				185					190			
146 Glu Ala 147	195			200					205				
150 Phe Gly 151 210			215					220					
154 Gly Ser 155 225		230					235					240	
158 Asp Asp 159		245				250					255		
162 Met Glu 163	260				265					270			
166 Ser Leu 167	275			280					285				
170 His Ala 171 — 290			295					300					
174 Leu Seu	Gly Gly	Gly Gly	Tyr	Thr	7.10	Arg	ñSI.	Val	Àla	Arg	Суз	Trp	

RAW SEQUENCE LISTING DATE: 02/27/2003 TATENT ARRIGINATION: US/09/645,337A TIME: 10:31:45

input Set : A:\104107.01.txt

Output Set: N:\CRF4\02272003\1645337A.raw

1.7 !;	3(,4:					310					315					32:0	
	Cys	Tyr	Glu	Thr		Val	A.a	Leu	G; À			Vai	G.J.	ASD	Lys	мет	
27 ±					325					330			<i>a</i> .	(3.1.)	335		
	Fre	Glu	His		ïуr	Tyr	Giu	Туг		G.y	1.1.0	ASP	. y :		Leu	ніѕ	
183				540					345		. 5		(1.7	350	1	C11	
	Val	Ala		Ser	ASI	Met	Glu		Lys	ASII	Ser	Arg		Me :	Leu	Glu	
187			355					360	_			7	365	(7.1		n 7 .	
	Glu		Arg	Asn	Asp	Leu		His	Asn	Leu	Ser		Leu	(all I	His	Ala	
191		370					375	_		5		380	C1."	m1	T'	(°.1	
		Ser	Val	Pro	Phe		G.u	Arg	Fro	Pro		Thr	G: U	Thr	Pro		
195		_				390			70		395	m	7	Disco	7	400	
	Val	Asp	Gitti	Asp		Gid	Asp	(1T À	Asp		Arg	rrp	ASD	Pro	Asp	ser	
199	_		_		405	-		70	,	410		¬	0	7	415	Tura	
	Asp	Met	Asp		Asp	Asp	Asp	Arg		Fro	LTE	Pro	ber		Val	гАг	
203		(2.1		420	63.3		70	ml.	425	7	·	Λ	01	430	Titro	Clu	
	Arg	Glu		Val	Gill	Pro	Asp		ьуѕ	ASD	нуѕ	ASD	- 445	ъец	Lys	(17 Å	
207			435		42.3	,	C1.7	440	03	3.7	C1	171		Clu	Com	010	
	11e		GIU	Arg	GIĀ	пЛВ		суѕ	G L d	V cl.	GIU	460	ирр	ULG	Ser	огу	
211	0	450	T	171	mil	C1	455	D. co. v.	I) was	57 · . 1	Clu		Clu	Clu	7. 12	Sor	
		:nr	ьуs	Val	1111	470	Vall	Z47213	1.10	Vcll	475	Val	GIU	GIU	Ala	480	
	465	7	Mat	c1	Clu		Civ	mik.v.	Acces	Luc		C1 v	Δ1ω	Clu	Gln		
	Vall	ьуѕ	Me t	ما بادی	485	GIU	('2 T Å	1111	нап	490	Оту	(3±Å	пта	OLG	495	nia	
219	Dha	Deco	Dro	T 170						· 1 .J ()					7 7 3		
223	rne	PTO	FIO	Lys 500	1111												
	201	n	FO 1:	D NO	• 3												
				H: 18													
			YPE:		000												
				ISM:	Aral	o i dor	osis	: ha	liana	ä							
			EATU		1., 0,	oraol	,010										
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				ION:													
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240	ťaa	aact:	t.gg i	gaat, a	agag	ag ac	gacte	ctga	g t.ga	agaga	agag	att	ctga	gt.g	agag	acggag	120
242	atg	gagge	cag .	acgaa	aagd	gg da	at.ct.	atat	g add	gtaga	ggac	dag	acgg	acg	t aag	cggcga	180
244	gta	agtt.	act.	totad	cgago	aa ga	acga:	t.agg.	a gad	atlaci	tact	acg	gtda	agg	ccad	cegatg	240
246	aag	cāta.	acc i	ggati	acgta	at go	gatic	atag	a ctv	aatc	at.t.c	act	at.ca	aat	ccac	ogtaga	300
248	t t.a	gaaa'	tica i	gtago	adati	ag co	aticg	etga	a ga	at.ac	gatā	tidg	godg	att.	ccat:	tagaag	360
250	gag:	tatg	ttg.	actt	actic	ga ti	tidagi	titit c	g cc	jgaa:	tata	tgg	gcga	t.ac	ttcc	gctgca	420
252	cga	aacci	taa	ggcga	attca	aa to	ytago	gtga	g gal	Litgti	actg	1.01	tcga	agg	actt	t.t.t.gat	480
254	t.t.t.	t.gda	gtg	atta	agaa	gg ac	ggtt	ctati	t. ggf	tgat	geog	tca	aatt	aaa	caga	caggac	540
																gattat	600
																tttaag	660
260	cgg	gt.t.c	tat i	adata	aga:	at to	gait.gr	ticcai	d dat	gga	gatig	gag	t.gga	aga	agdg	ttttac	720
262	acca	actiga	ata i	gagti	tato	ac to	gt.tit (ottt:	3 Pas	Jaraan	: *. t q	ddd	act t	ttt	gddai	ggaact	780
264	ggt	cacai	taa -	gagai	tgtt	gg c	gat ga	dada	a gg	Jada'i	tart.	atg	atat	add	tigt ti	ccacta.	840
266	aac	gatg	gta :	t ggav	agat	ja a	aqtt:	: तत्रव	3 aQ	** 1.g	1.1.d	다리다	at at	t, /a f	ccag	aaggt t.	900

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Output Set: N:\CRF4\02272003\1645337A.raw

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26% atggaagtgt afcagcoaga ggoagtigtt etfoagtgty gigoigacic oftaagtggt
    270 gateggitigg gittgetteau ettaleagte augggicaeg elgaligeet leggifetfa.
                                                                          1000
    272 againthana angithesin: Paiggigily ggigglyaag ggialaniat togaaatgit
                                                                          7.020
    274 genegtiget ggryftatga gaergeagit gelyttagag tagageegga caacaaaefe
                                                                          -1140
    276 cottacaatg agtaittiga glattioggo coagailata ogottoatgt oganocaagt
                                                                          1200
                                                                          1260
    278 octatggaga attiaaacac goocaaagat atggagagga taaggaacac giigciyyaa
    280 carettiegg gaetaatada egeaectage giocagitte ageaeacace accagicaat
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                                                                           1380
W--> 282 cgagttttgg acgageegga agatgaeatg gagaeaagae caaaaeeteg eatntggagt
    284 ggaactgcga ettatgaate agacagtgae gatgatgata aacetettea tggttaetea
    286 tgtogtggtg gogcaactae ggacagggad totacoggtg aagatgaaat ggatgacgat
                                                                          1500
                                                                           1560
    288 aacccagage cagacgtgaa tectecateg tettaaacca gettgatggt ttggtgtete
    290 tittgecata tgataatgic ggcagattta agaaacaagt taggggaatg aatgatteit
                                                                           1620
                                                                           1680
    292 igaigittit toagoaacci tilgagitet gigaaaacgo igcatigati agaacagiga
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                    20
    320 Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His Arg Ile Arg Met Ala
                                                       45
                                   40
                35
     324 His Ser Leu Ile Ile His Tyr His Leu His Arg Arg Leu Glu Ile Ser
                                55
     328 Arg Pro Ser Leu Ala Asp Ala Ser Asp Ile Gly Arg Phe His Ser Pro
                                               75
                            70
    332 Glu Tyr Val Asp Phe Lou Ala Sor Val Ser Pro Glu Sor Met Gly Asp
                        8.5
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     336 Pro Ser Ala Ala Arg Asn Leu Arg Arg Phe Asn Val Gly Glu Asp Cys
                                       105
                                                           110
     337 100
     340 Pro Val Phe Asp Gly Leu Fhe Asp Phe Cys Arg Ala Ser Ala Gly Gly
        115
                                   120
     344 Ser lle Gly Ala Ala Val Lys Leu Asn Arg Gln Asp Ala Asp Ile Ala
                                                   1.40
                                135
     345 130
     348 Ile Asn Trp Gly Gly Gly Lea His His Ala Lys Lys Ser Glu Ala Ser
                            150
                                               155
     349 145
    352 Gly Phe Cys Tyr Val Asn Asp lie Val Leu Gly He Leu Glu Leu Leu
                                           170
     356 Lys Met. Phe Lys Arg Val Leu Tyr lie Asp Ile Asp Val His His Gly
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                    180
     360 Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg Vai Met Thr Val
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RAW SEQUENCE LISTING

PATENT AFFEICATION: US/09/645,337A

DATE: 0272772003 TIME: 10:31:45

Input Set : A:\104107.01.txt

Output Set: N:\CRF4\02272003\1645337A.raw

	601			195					200					205				
		Ser	Hite	His	Lvs	His	Glv	Asp	Pho	Flie	Pro	СТУ	Thr	G1v	His	11.	Ar ī	
			2.10		1		-	215				-	220	•				
					Λ	(11 in	100			TUVE	TVE	15 i K		Ash	Val	Pro	Lea	
		225	V (1 .	:	11(4	020	230	· · - y	2 · y	- 1 -	. , .	235					240	
			T	27.1 · · ·	\$4 ±.	T		C	C1	151	N 60 00			E. leaze	Deca	Lowers		
		ASII	Asp	ыТА	Met		ASD	Gr. U	b⊕r	File		Ser	r.eu	PIIG	Mr.g		LINE CAL	
	573					245					250					255		
3	376	lle	Glri	Lys		Met	Giu	Val			Pro	Glu	Ala	Va1	Vāl	Leu	GIn	
	377				260					265					270			
3	380	Cys	Gly	Ala	Asp	Ser	Leu	Ser	Gly	Asp	Arg	Leu	Gly	Cys	Phe	Asn	Leu	
3	381			275					280					285				
3	384	Ser	Val	Lys	Gly	His	Ala	Asp	Cys	Leu	Arg	Phe	Leu	Arg	Ser	Tyr	Asn	
	385			•				295	-				300					
3	888	Val				Va1	Leu	Glv	Glv	Glu	Glv	Tyr	Thr	Tie	Ara	Asn	Val	
		305		201.0			310		= .1		- 1	315			,		320	
			A vice	Cue	m vr.	Cura		Glu	Thr	Ala	Wa.	Ala	Val	Glv	V1	Gla		
		MIG	ni g	C y S	1112	325	1 Y	O1 U	1	711(1	330	7.1.4	V (3.1	() <u>1</u> . y		335	* * ·	
	393	70		,	,		П'	T	C1	т		(2.3 v.	m	734.00	C1		Dir	
		Asp	ASII	ьуѕ		rro	туг	ASII	GTU		:TIE	Glu	тУĽ	rne		FIU	Web	
	397				340					345			_		350	****	**	
4	100	Тут	Thr		His	Val	Asp	Pro		Pro	Met	Glu	Asn		Asn	Thr	Pro	
	01			355					360					365				
4	104	Lys	Asp	Met	Glu	Arg	Ι1€	Arg	Asn	Thr	Leu	Leu	Glu	Gln	Leu	Ser	G1 A	
			370					375					380					
	105										4 4 14	D 1 -	(*) 1	T-	TT.	* * T	7)	
4		Leu	Ile	His	Ala	Pro	Ser	Va1	Gln	Phe	Gin	HIS	unr	Pro	Pro	Val	ASH	
4 4	108	Leu 385	Ile	His	Ala	Pro	Ser 390	Val	Gln	Phe	Gin	ил s 395	hnr	Pro	Pro	Val	400	
4 4 4	108 109	385					390					395					400	
4 4 4 4	108 109 112	385				Glu	390										400	
4 4 4 4	108 109 112 113	385 Arg	Val	Leu	Asp	Glu 405	390 Pro	Glu	Asp	Asp	Met 410	395 Glu	Thr	Arg	Pro	Lys 415	400 Pro	
4 4 4 4 w> 4	108 109 112 113	385 Arg	Val	Leu	Asp Ser	Glu 405	390 Pro	Glu	Asp	Asp Tyr	Met 410	395 Glu	Thr	Arg	Pro Asp	Lys 415	400 Pro	
4 4 4 4 4 w> 4	108 109 112 113 116	385 Arg Arg	Val Xaa	Leu Trp	Asp Ser 420	Glu 405 Gly	390 Pro	Glu Ala	Asp Thr	Asp Tyr 425	Met 410 Glu	395 Glu Ser	Thr Asp	Arg Ser	Pro Asp 430	Lys 415 Asp	400 Pro Asp	
4 4 4 W> 4 4 4	108 109 112 113 116 117	385 Arg Arg	Val Xaa	Leu Trp Pro	Asp Ser 420	Glu 405 Gly	390 Pro	Glu Ala	Asp Thr Ser	Asp Tyr 425	Met 410 Glu	395 Glu	Thr Asp	Arg Ser Ala	Pro Asp 430	Lys 415 Asp	400 Pro Asp	
4 4 4 4 4 4	108 109 112 113 116 117 120	385 Arg Arg Asp	Val Xaa Lys	Leu Trp Pro 435	Asp Ser 420 Leu	Glu 405 Gly His	390 Pro Thr Gly	Glu Ala Tyr	Asp Thr Ser 440	Asp Tyr 425 Cys	Met 410 Glu Arg	395 Glu Ser Gly	Thr Asp Gly	Arg Ser Ala 445	Pro Asp 430 Thr	Lys 415 Asp Thr	400 Pro Asp Asp	
4 4 4 4 4 4 4 4	108 109 112 113 116 117 120 121	385 Arg Arg Asp	Val Xaa Lys Asp	Leu Trp Pro 435	Asp Ser 420 Leu	Glu 405 Gly His	390 Pro Thr Gly	Glu Ala Tyr Asp	Asp Thr Ser 440	Asp Tyr 425 Cys	Met 410 Glu Arg	395 Glu Ser	Thr Asp Gly Asp	Arg Ser Ala 445	Pro Asp 430 Thr	Lys 415 Asp Thr	400 Pro Asp Asp	
4 4 4 4 4 4 4 4 4 4 4 4 4	108 109 112 113 116 117 120 121 124	385 Arg Arg Asp	Val Xaa Lys Asp 450	Leu Trp Pro 435 Ser	Asp Ser 420 Leu Thr	Glu 405 Gly His	390 Pro Thr Gly	Glu Ala Tyr Asp 455	Asp Thr Ser 440	Asp Tyr 425 Cys	Met 410 Glu Arg	395 Glu Ser Gly	Thr Asp Gly	Arg Ser Ala 445	Pro Asp 430 Thr	Lys 415 Asp Thr	400 Pro Asp Asp	
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	108 109 112 113 116 117 120 121 124 128 132 133 134 135 137	385 Arg Arg Asp Asp 465 <210 <211 <211 <400	Val Xaa Lys Asp 450 Val 0> SH 1> LH 2> TY 8> OH 0> SH	Leu Trp Pro 435 Ser Asn EQ II ENGTH (PE: RGAN)	Asp Ser 420 Leu Thr Pro D NO: DNA ISM: NCE:	Glu 405 Gly His Gly Pro 539	390 Pro Thr Gly Glu Ser 470	Glu Ala Tyr Asp 455 Ser	Asp Thr Ser 440 Glu	Asp Tyr 425 Cys Met	Met 410 Glu Arg Asp	395 Glu Ser Gly Asp	Thr Asp Gly Asp 460	Arg Ser Ala 445 Asn	Pro Asp 430 Thr	Lys 415 Asp Thr Glu	400 Pro Asp Asp Pro	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	108 109 112 113 116 117 120 121 124 125 128 133 134 135 137 138	385 Arg Arg Asp Asp 465 <210 <211 <400 cace	Val Xaa Lys Asp 450 Val 0> SH 1> LH 1> CH 1> CH 1- CH	Leu Trp Pro 435 Ser Asn EQ II ENGTH (PE: RGAN) EQUEN	Asp Ser 420 Leu Thr Pro D NO: H: 90 DNA ISM: NCE:	Glu 405 Gly His Gly Pro 539 Aral 5	390 Pro Thr Gly Glu Ser 470	Glu Ala Tyr Asp 455 Ser	Asp Thr Ser 440 Glu	Asp Tyr 425 Cys Met	Met 410 Glu Arg Asp	395 Glu Ser Gly Asp	Thr Asp Gly Asp 460	Arg Ser Ala 445 Asn	Pro Asp 430 Thr Pro	Lys 415 Asp Thr Glu	400 Pro Asp Asp Pro	60
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	108 109 1112 1113 116 1117 120 121 124 125 128 128 133 134 135 137 138 140	385 Arg Arg Asp Asp 465 <210 <211 <400 cace	Val Xaa Lys Asp 450 Val 0> SH 1> LH 1> CH 1> SH 1> SH 1- SH	Leu Trp Pro 435 Ser Asn EQ II ENGTH (PE: RGAN: EQUE: EQUE: EQUE EQUE EQUE EQUE EQUE E	Asp Ser 420 Leu Thr Pro D NO: H: 90 DNA ISM: NCE: Laaaa	Glu 405 Gly His Gly Pro 539 Aral 5	390 Pro Thr Gly Glu Ser 470	Glu Ala Tyr Asp 455 Ser	Asp Thr Ser 440 Glu thal	Asp Tyr 425 Cys Met	Met 410 Glu Arg Asp	395 Glu Ser Gly Asp	Thr Asp Gly Asp 460	Arg Ser Ala 445 Asn	Pro Asp 430 Thr Pro	Lys 415 Asp Thr Glu	400 Pro Asp Asp Pro .tctgq cttatc	120
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	108 109 1112 1113 116 1117 120 121 124 125 128 128 133 134 135 137 138 140	385 Arg Arg Asp Asp 465 <210 <211 <400 cace	Val Xaa Lys Asp 450 Val 0> SH 1> LH 1> CH 1> SH 1> SH 1- SH	Leu Trp Pro 435 Ser Asn EQ II ENGTH (PE: RGAN: EQUE: EQUE: EQUE EQUE EQUE EQUE EQUE E	Asp Ser 420 Leu Thr Pro D NO: H: 90 DNA ISM: NCE: Laaaa	Glu 405 Gly His Gly Pro 539 Aral 5	390 Pro Thr Gly Glu Ser 470	Glu Ala Tyr Asp 455 Ser	Asp Thr Ser 440 Glu thal	Asp Tyr 425 Cys Met	Met 410 Glu Arg Asp	395 Glu Ser Gly Asp	Thr Asp Gly Asp 460	Arg Ser Ala 445 Asn	Pro Asp 430 Thr Pro	Lys 415 Asp Thr Glu	400 Pro Asp Asp Pro .tctgq cttatc	
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	108 109 1112 1113 116 117 120 121 124 125 128 129 133 134 135 137 138 140 142	385 Arg Arg Asp Asp 465 <210 <211 <400 dacq ggaa cacc	Val Xaa Lys Asp 450 Val >> SH >> CH >> CH >> CH >> CH >> CH	Leu Trp Pro 435 Ser Asn EQ II ENGTH (PE: RGAN: EQUE: EGG ! EGG !	Asp Ser 420 Leu Thr Pro D NO: H: 90 DNA ISM: NCE: Laaaa	Glu 405 Gly His Gly Pro 539 Aral 6	390 Pro Thr Gly Glu Ser 470	Glu Ala Tyr Asp 455 Ser osis	Asp Thr Ser 440 Glu thal	Asp Tyr 425 Cys Met	Met 410 Glu Arg Asp	395 Glu Ser Gly Asp	Thr Asp Gly Asp 460	Arg Ser Ala 445 Asn	Pro Asp 430 Thr Pro	Lys 415 Asp Thr Glu	400 Pro Asp Asp Pro Ctctgq Ctctate Scttta	120
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1408 1409 1412 1413 1416 1417 1420 1421 1424 1425 1428 1429 1432 1433 1440 1442 1444	385 Arg Arg Asp Asp 465 <210 <210 <400 dacd dacd dacd catc	Val Xaa Lys Asp 450 Val > SE > SE > SE gogto attgatta	Leu Trp Pro 435 Ser Asn EQ II ENGTE (PE: RGANE EQUE: ECG : ECG : ECG total	Asp Ser 420 Leu Thr Pro DNO: H: 90 DNA ISM: Laaaa Ltaaaa Ltaaa	Glu 405 Gly His Gly Pro 539 Arak 5 aatco	390 Pro Thr Gly Glu Ser 470 pidor of ct gg as fit to	Ala Tyr Asp 455 Ser osis cett:	Asp Thr Ser 440 Glu thal ittet cagti	Asp Tyr 425 Cys Mot. Lana car acr	Met 410 Glu Arg Asp	395 Glu Ser Gly Asp	Thr Asp Gly Asp 460	Arg Ser Ala 445 Asn	Pro Asp 430 Thr Pro	Lys 415 Asp Thr Glu gagt agtg gagt	400 Pro Asp Asp Pro .tctgq cttate .ccttta atccct	120 180
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1408 1409 1412 1413 1416 1417 1420 1421 1424 1425 1428 1429 1432 1433 1440 1442 1444 1446	Arg Arg Asp Arg Asp 465 <210 <211 <400 cacc ggaa cacc cagc	Val Xaa Lys Asp 450 Val > SE > CF gcgtcattgatttcgttaaa	Leu Trp Pro 435 Ser Asn EQ II ENGTR (PE: EGANE EQUE EGG t eag t eag t eat a	Asp Ser 420 Leu Thr Pro NO: DNA ISM: Caaaa Ctaaaa Ctaaaa Ctaggca	Glu 405 Gly His Gly Pro 539 Aral 5 actor ator ator ator ator ator ator ator a	390 Pro Thr Gly Glu Ser 470 pidor at ct gg as it to a ga gt at	Ala Tyr Asp 455 Ser esis cett: aagco jgagaactt	Thr Ser 440 Glu thal ittet cagti aatigt ggtt	Asp Tyr 425 Cys Mot. Lana car acri acri acri gas	Met 410 Glu Arg Asp accti accti accti accti accti accti accti	395 Glu Ser Gly Asp tgat acto aaga acto gago	Thr Asp Gly Asp 460	Arg Ser Ala 445 Asn	Pro Asp 430 Thr Pro cat cagg caggt to tage cag to tage cagg cagg cagg cagg cagg cagg cagg c	Lys 415 Asp Thr Glu gagt catto igtgo jaada itggo	400 Pro Asp Asp Pro Ctotgg Ctotgg Ctate Cottate Cottata Atcoct Ggaaaa	120 180 240
## 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1408 1409 1412 1413 1416 1417 1420 1421 1424 1425 1428 1429 1432 1433 1440 1444 1446 1448	Arg Arg Asp Asp 465 <210 <210 <210 cacc ggaa cacc cagc ggaa ggaa	Values Lys Asp 450 Val > SE > TY SS of the second seco	Leu Trp Pro 435 Ser Asn EQ II ENGTH (PE: CGG ! Edg to Edg	Asp Ser 420 Leu Thr Pro D NO: H: 9' DNA ISM: (aaaa (taaaa (taaaa) (taaaa) (taaaa) (taaaa) (taaaa) (taaaa)	Glu 405 Gly His Gly Pro 539 Aral 5 acticacatic	390 Pro Thr Gly Glu Ser 470 oidor at ct gg as gg as	Ala Tyr Asp 455 Ser ctt: aagcoggagaactt	Thr Ser 440 Glu thal ttet cagti aatgt ggtt acaac	Asp Tyr 425 Cys Mot. iiana dar aca aca coti	Met 410 Glu Arg Asp accti accti actg aaaca gggaa gtttc	395 Glu Ser Gly Asp tgat actc aaga actc gagc ittg	Thr Asp Gly Asp 460	Arg Ser Ala 445 Asn	Pro Asp 430 Thr Pro cat cagg caggtt taga cagg	Lys 415 Asp Thr Glu gagt catto igtgo gaada itggo ctatt	Asp Asp Pro Pro Asp	120 180 240 300 360
## 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1408 1409 1412 1413 1416 1417 1420 1421 1424 1425 1428 1429 1432 1433 1440 1444 1446 1448 1446 1448	Arg Arg Asp Asp 465 <210 <210 <210 cacc ggaa cacc cagc ggaa gaac	Values Lys Asp 450 Val > SE > The post of the post	Leu Trp Pro 435 Ser Asn EQ II ENGTH (PE: RGAN) Tog : tite a agg t ct. c. tt. a	Asp Ser 420 Leu Thr Pro D NO: H: 90 DNA ISM: Laaaa Ltaaaa Ltaaaa Ltaaaa Ltaaaa Ltaaaa Ltaaaa Ltaaaa	Glu 405 Gly His Gly Pro 539 Aral 5 acticaçatogo atogo atogo gaaco attgo	390 Pro Thr Gly Glu Ser 470 oidor it ct gg ac gg	Ala Tyr Asp 455 Ser ctt: aggoggagaactt tcgaactt	Thr Ser 440 Glu thal thal ittet cagti aatgt icaacg icaact icac	Asp Tyr 425 Cys Mot. Lana Lana Lana Lana Lana Lana Lana Lan	Met 410 Glu Arg Asp accti acti acti acti acti acti acti ac	395 Glu Ser Gly Asp tgat actc aaga actc gago attg	Thr Asp Gly Asp 460	Arg Ser Ala 445 Asn Asn	Pro Asp 430 Thr Pro cat cagg caggtt taga cagg cagg cagg cagg	Lys 415 Asp Thr Glu gagt catto gtgc gaaca tggc ctatt gtat	Asp Asp Pro Pro Asp Asp Pro Asp Cttagg Cttate Ccttta Atccct Ggaaaa Ctgag Gctaaa	120 180 240 300 360 420
## 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	408 409 4112 4113 4116 4120 4121 4124 4125 4128 4128 4129 4133 4133 4140 4144 4146 4148 4150 4150	Arg Arg Asp Arg Asp 465 <210 <211 <400 cacc cacc cagc cacc cagc cacc cagc cacc cagc	Values Lys Asp 450 Val > SE > TY SE gcgtc gtaas gtttc gtaas tttt gaaga	Leu Trp Pro 435 Ser Asn EQ II ENGTH (PE: RGAN) SQUE: tcg : tcc a agg t ctc a agg t ctc a	Asp Ser 420 Leu Thr Pro D NO: DNA ISM: Caaaa aggca attggc gtgat acttf aagac agcof	Glu 405 Gly His Gly Pro 39 Aral 5 39 Aral 6 30 acceptogo (ttgo (390 Pro Thr Gly Glu Ser 470 Didor t ct grade t to a grade grad grade grade grade grade grade grade grade grade grade grade grade grade grade grade grad grade grade grade grade grade grade grad grade grad grade grade grade grade grad grade grad grad grad grad grad grade grade grade grad grad grad grad grad grad grad grad	Ala Tyr Asp 455 Ser sis ctt: aggegaactt tega actt tega gaagt	Thr Ser 440 Glu thal thal tret cagtt cagtt acaac acaac acaac	Asp Tyr 425 Cys Met Lana Lac acc acc gas cocc gas	Met 410 Glu Arg Asp Asp accidents aggas gutto tauti .gggs .ggtto	395 Glu Ser Gly Asp tgat actc aaga actc gatg gatg	Thr Asp Gly Asp 460 tott ctga agg tata tata age ctga at age at age age age age age age age age	Arg Ser Ala 445 Asn aggae aggae ctacae ccace	Pro Asp 430 Thr Pro cat cagg caggt to tage tagg cagg tagg tagg tagg tagg tagg tagg	Lys 415 Asp Thr Glu gagt tatte gage ttge ttge ttgage	Asp Asp Pro Pro Asp	120 180 240 300 360

RAW SEQUENCE LISTING ERROR SUMMARY
FATERT AFFLICATION: US/09/645,337A

DATE: 02/03/2003 TIME: 10:31:46

Input Set : A:\104107.01.txt

Output Set: N:\CRF4\02272003\1645337A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1374
Seq#:4; Xaa Pos. 418

VERIFICATION SUMMARY

HATENT APPLICATION: US/09/645,337A TIME: 10:31:46

DATE: 02/27/2003

Input Set : A:\104107.01.txt

Output Set: N:\CRF4\02272003\I645337A.raw

L:282 M:341 W: (46) "n" or "Xaa" used, for SEQ !D#:3 after pos.:1320 1:416 Mi34) W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:416